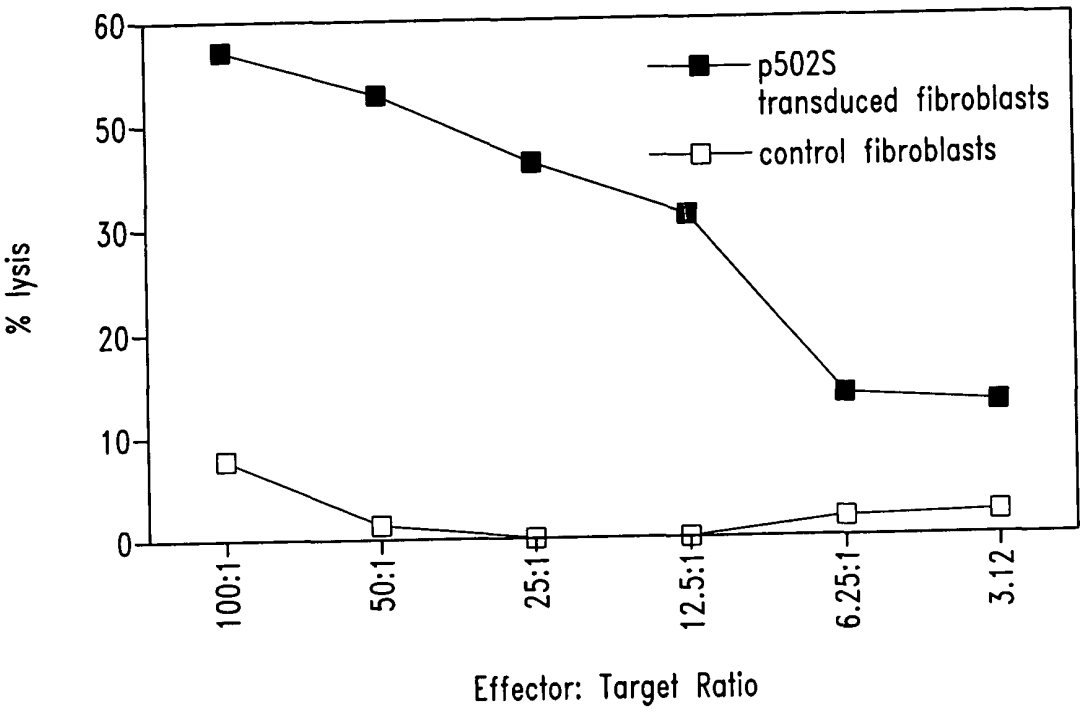

60
50
30
20
10
0
% lysis
p502S
transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

Fig. 1

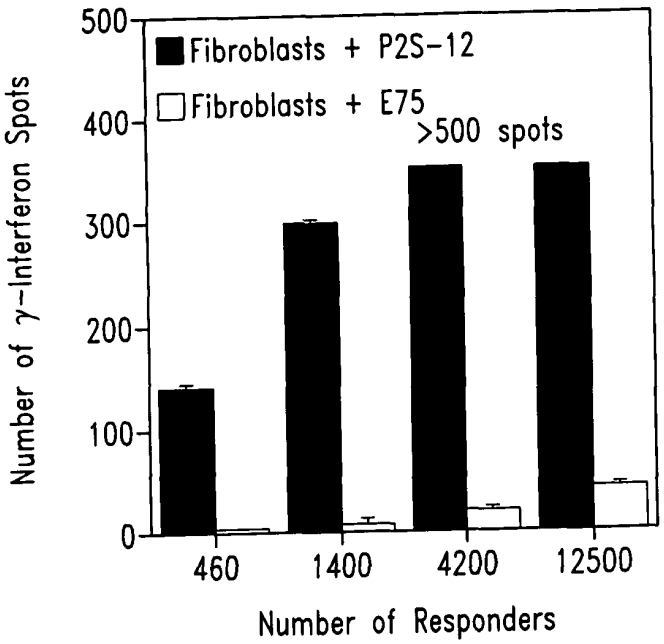

Fibroblasts + P2S-12
Fibroblasts + E75
>500 spots
Number of γ-Interferon Spots
500
400
300
200
100
0
460
1400
4200
12500
Number of Responders

Fig. 2A

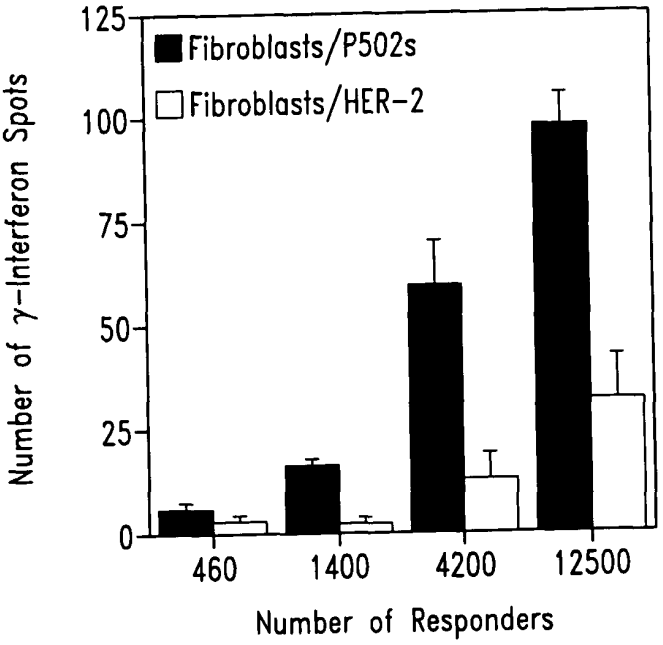

Fibroblasts/P502s
Fibroblasts/HER-2
Number of γ-Interferon Spots
125
100
75
50
25
0
460
1400
4200
12500
Number of Responders

Fig. 2B

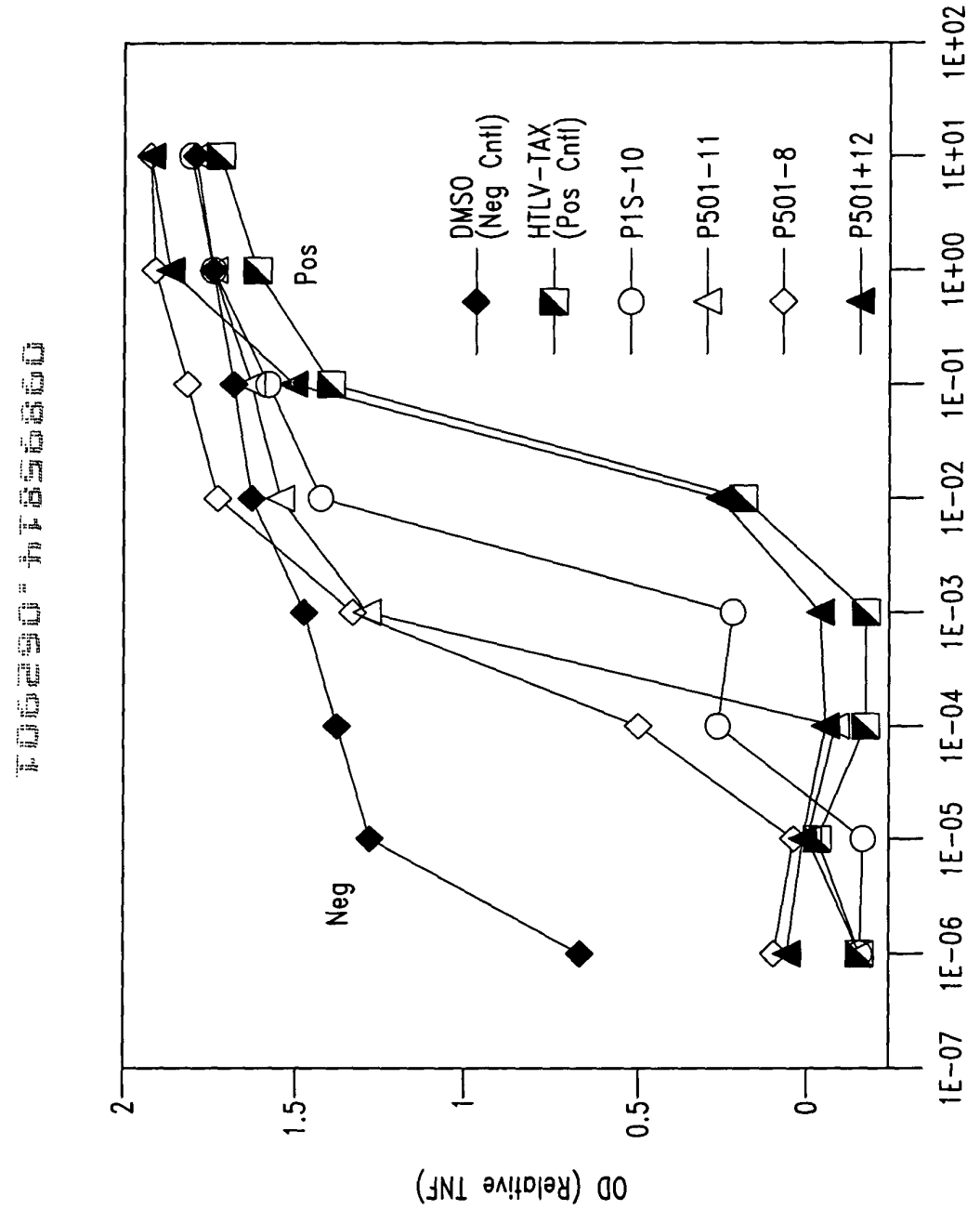

OD (Relative TNF)
2
1.5
1
0.5
0
1E-07
1E-06
1E-05
1E-04
1E-03
1E-02
1E-01
1E+00
1E+01
1E+02
[fluM58] ug/ml
Neg
Pos
DMSO (Neg Cntl)
HTLV-TAX (Pos Cntl)
P1S-10
P501-11
P501-8
P501+12

Fig. 3

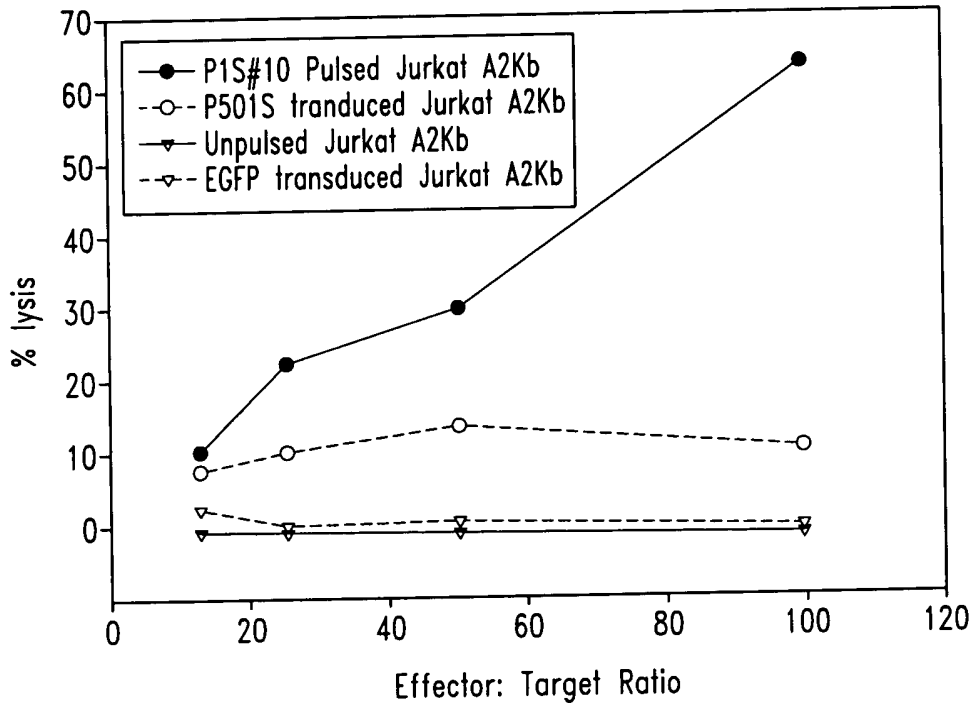

P1S#10 Pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
Unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
0
10
20
30
40
50
60
70
0
20
40
60
80
100
120

Fig. 4

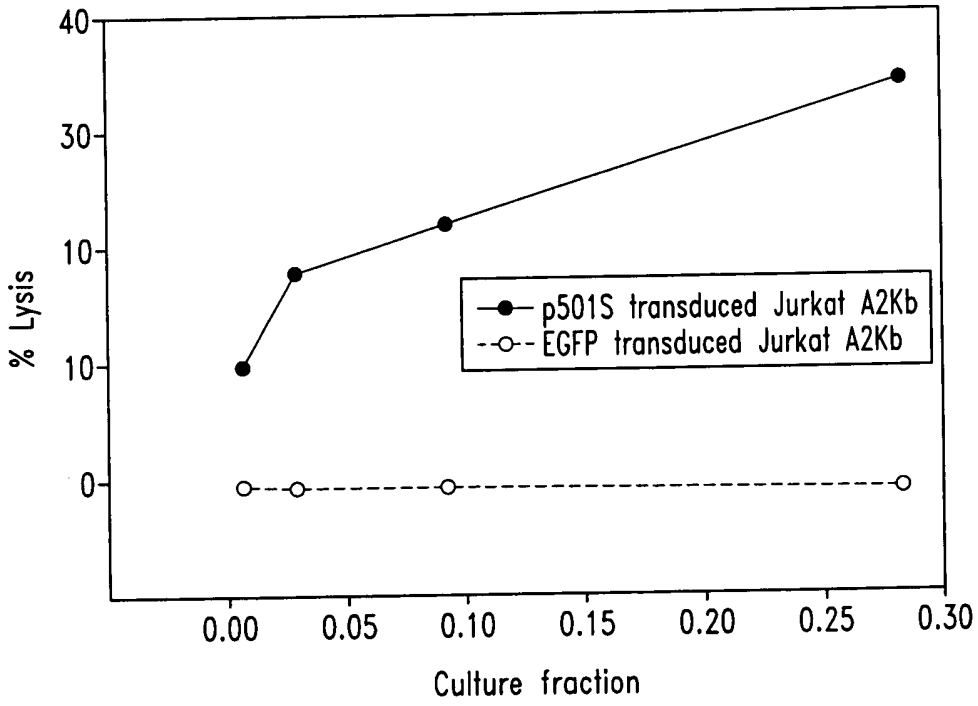

p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% Lysis
Culture fraction
0
10
10
30
40
0.00
0.05
0.10
0.15
0.20
0.25
0.30

Fig. 5

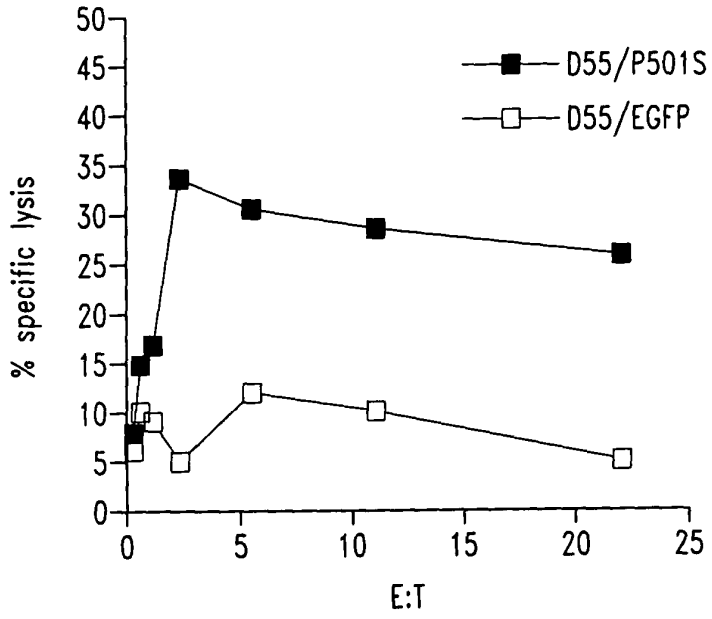

D55/P501S
D55/EGFP
% specific lysis
E:T
0
5
10
15
20
25
30
35
40
45
50

Fig. 6A

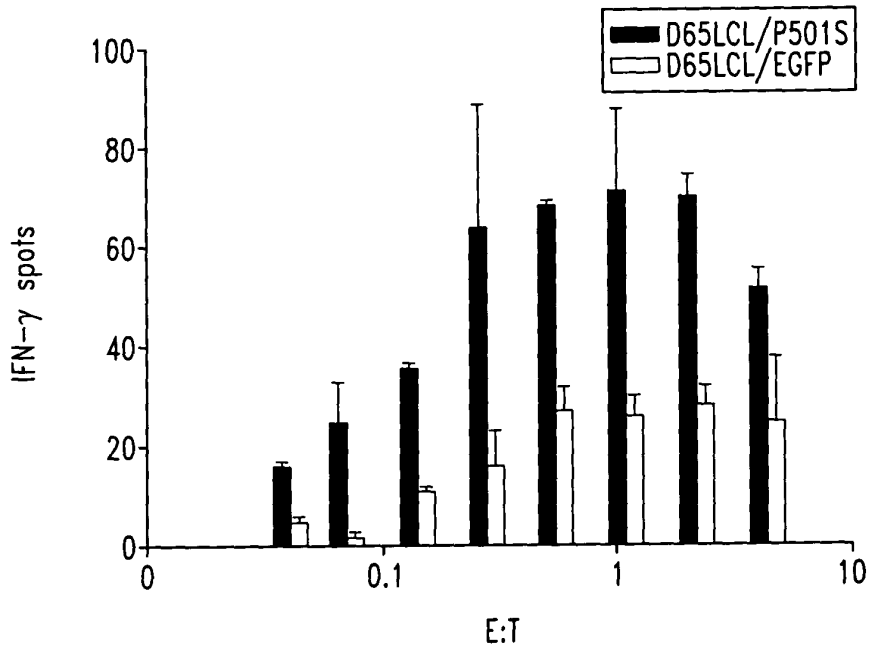
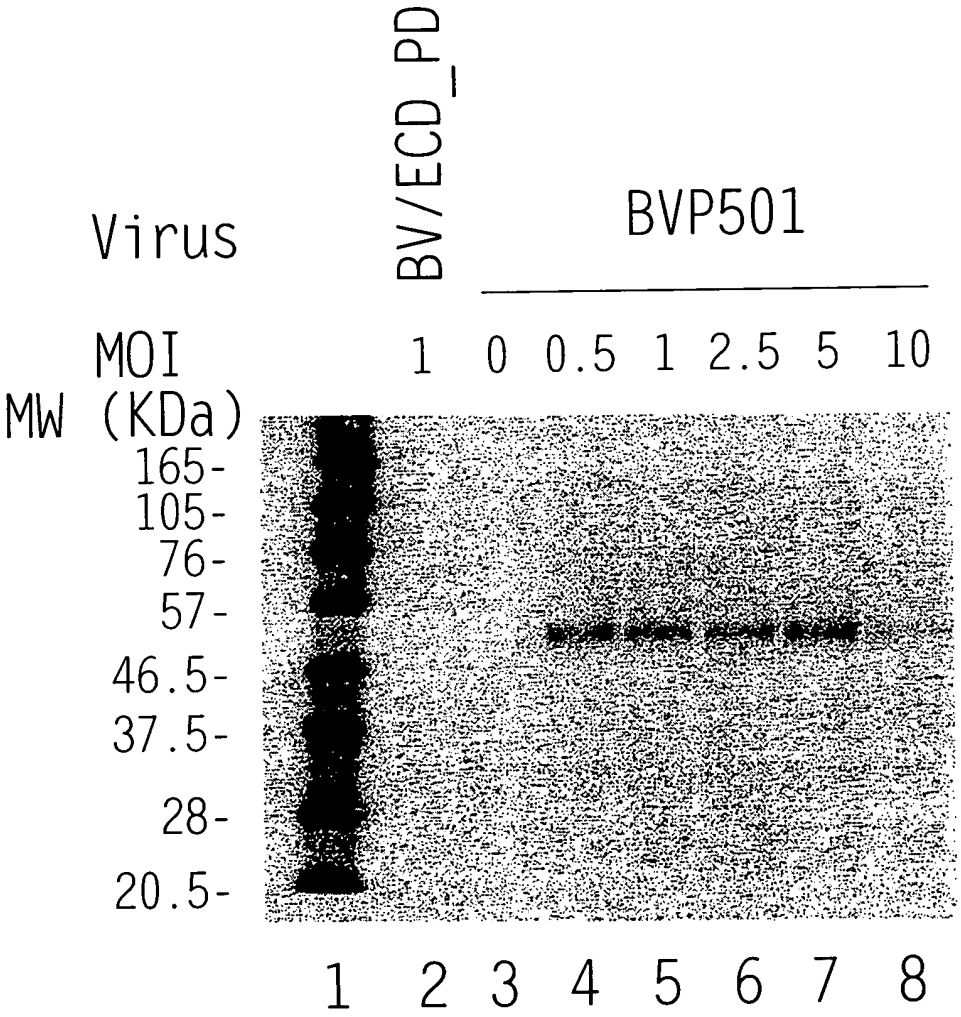

D65LCL/P501S
D65LCL/EGFP
IFN-γ spots
E:T
0
20
40
60
80
100
0
0.1
1
10

Fig. 6B

Expression of P501S
by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3

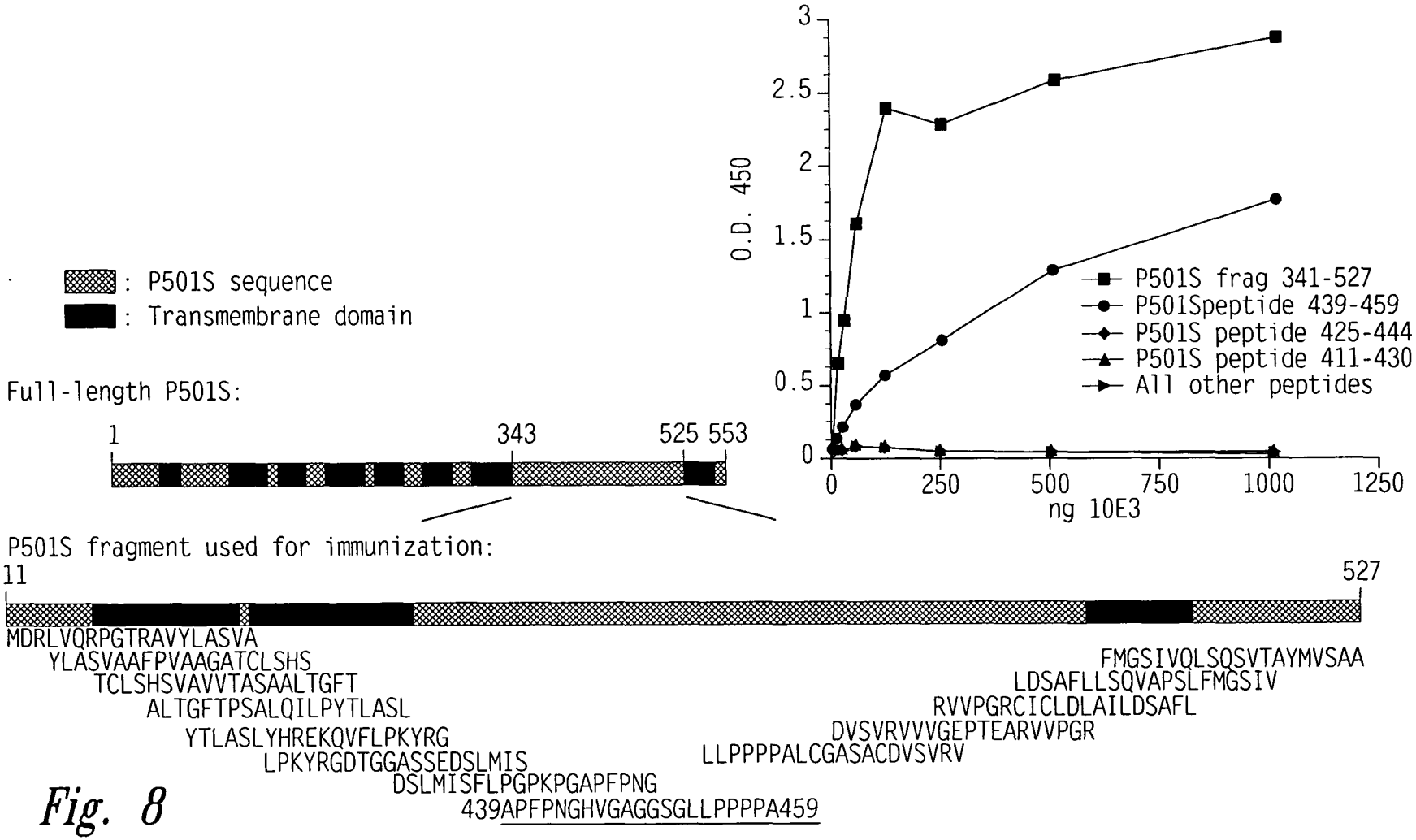


Fig. 8

Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER
Inventor(s): Jia[redacted]n Xu et al. Serial No.
Do[redacted]No. 210121.427C26

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLEVGVEEKFM**
TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL **AGLLCPDPRPLE** LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI **DWDTSALAPYLGTQEE**

CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF **VGEGLYQGVPRAEPGTEARRHYDEGVR**

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady an I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9

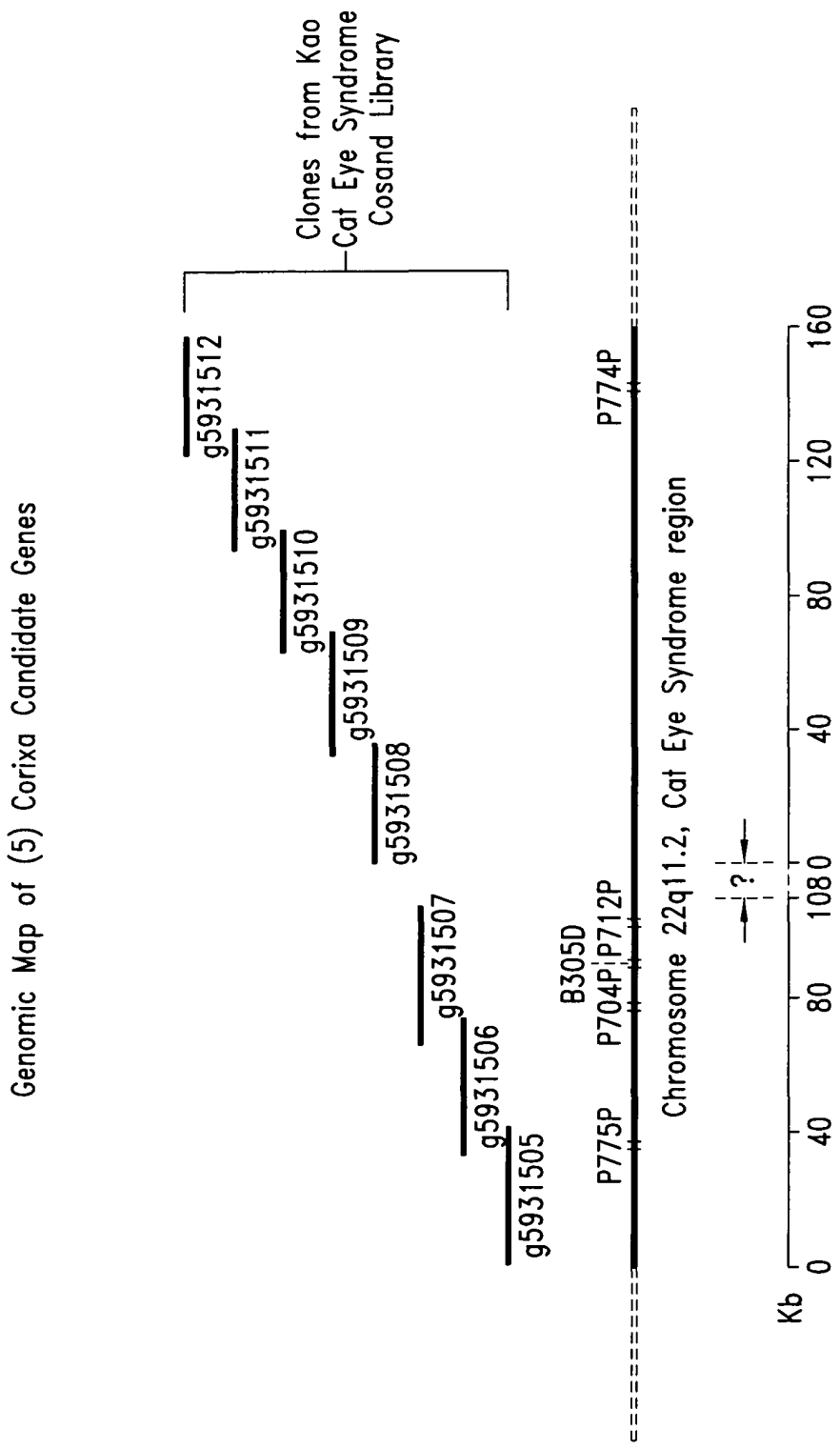

Genomic Map of (5) Corixa Candidate Genes
Clones from Kao
Cat Eye Syndrome
Cosand Library
g5931512
g5931511
g5931510
g5931509
g5931508
g5931507
g5931506
g5931505
P774P
B305D
P704P
P712P
P775P
Chromosome 22q11.2, Cat Eye Syndrome region
?
Kb
0
40
80
108 0
40
80
120
160

Fig. 10

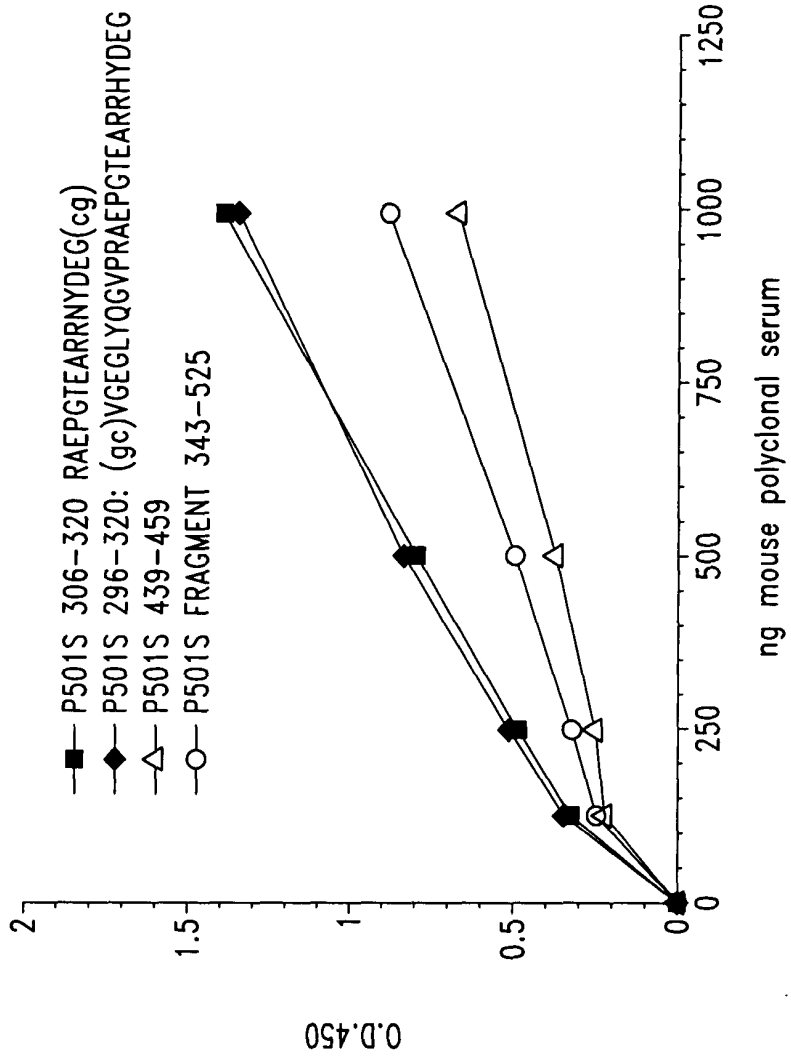

Elisa assay of rabbit polyclonal antibody specificity
P501S 306-320 RAEPGTEARRNYDEG(cg)
P501S 296-320: (gc)VGEGLYQGVPRAEPGTEARRHYDEG
P501S 439-459
P501S FRAGMENT 343-525
O.D.450
ng mouse polyclonal serum
0
0.5
1
1.5
2
0
250
500
750
1000
1250

Fig. 11